

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.**

Application Serial Number: 10/807,228A
Source: 1FW16
Date Processed by STIC: 4/27/05

ENTERED



IFW16

RAW SEQUENCE LISTING

DATE: 04/27/2005

PATENT APPLICATION: US/10/807,228A

TIME: 14:06:54

Input Set : A:\226749.st25 Replacement Sequence Listing.txt

Output Set: N:\CRF4\04272005\J807228A.raw

SEQUENCE LISTING

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3 (1) GENERAL INFORMATION:
5     (i) APPLICANT: Sogabe, Atsushi
6           Hattori, Takashi
7           Nishiya, Yoshiaki
8           Kawamura, Yoshihisa
10    (ii) TITLE OF INVENTION: Creatine Amidinohydrolase, Production
11           Thereof and Use Thereof
C--> 13    (iii) NUMBER OF SEQUENCES: 3
15    (iv) CORRESPONDENCE ADDRESS:
16           (A) ADDRESSEE: LEYDIG, VOIT & MAYER, LTD.
17           (B) STREET: Two Prudential Plaza, Suite 4900
18           (C) CITY: Chicago
19           (D) STATE: Illinois
20           (E) COUNTRY: USA
21           (F) ZIP: 60601-6780
23    (v) COMPUTER READABLE FORM:
24           (A) MEDIUM TYPE: Diskette - 3.5 inch, 1.44 Mb storage
25           (B) COMPUTER: IBM PC compatible
26           (C) OPERATING SYSTEM: PC-DOS/MS-DOS
27           (D) SOFTWARE:
29    (vi) CURRENT APPLICATION DATA:
C--> 30           (A) APPLICATION NUMBER: US/10/807,228A
C--> 31           (B) FILING DATE: 23-Mar-2004
32           (C) CLASSIFICATION: Divisional
34    (vii) PRIOR APPLICATION DATA:
35           (A) APPLICATION NUMBER: JP 25435/1996
36           (B) FILING DATE: 13-FEB-1996
38    (viii) ATTORNEY/AGENT INFORMATION:
39           (A) NAME: John Kilyk, Jr.
40           (B) REGISTRATION NUMBER: 30,763
C--> 41           (C) REFERENCE/DOCKET NUMBER: 226749
43    (ix) TELECOMMUNICATION INFORMATION:
44           (A) TELEPHONE: (312) 616-5600
45           (B) TELEFAX: (312) 616-5700
46           (C) TELEX: 25-3533
48 (2) INFORMATION FOR SEQ ID NO: 1:
50     (i) SEQUENCE CHARACTERISTICS:
51           (A) LENGTH: 404 amino acids
52           (B) TYPE: amino acid
53           (D) TOPOLOGY: linear
W--> 55     (ii) MOLECULE TYPE:
56           (A) DESCRIPTION: protein

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58      (vi) ORIGINAL SOURCE:
59          (A) ORGANISM: Alcaligenes faecalis
60          (B) STRAIN: TE3581 (FERM P-14237)
62      (ix) FEATURE:
63          (A) NAME/KEY: mat peptide
64          (B) LOCATION: 1 to 404
65          (D) OTHER INFORMATION: protein having creatine amidino-
66 hydrolase activity
68      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
70 Met Thr Asp Asp Met Leu His Val Met Lys Trp His Asn Gly Glu Lys
71 1      5      10      15
72 Asp Tyr Ser Pro Phe Ser Asp Ala Glu Met Thr Arg Arg Gln Asn Asp
73      20      25      30
74 Val Arg Gly Trp Met Ala Lys Asn Asn Val Asp Ala Ala Leu Phe Thr
75      35      40      45
76 Ser Tyr His Cys Ile Asn Tyr Tyr Ser Gly Trp Leu Tyr Cys Tyr Phe
77      50      55      60
78 Gly Arg Lys Tyr Gly Met Val Ile Asp His Asn Asn Ala Thr Thr Ile
79      65      70      75      80
80 Ser Ala Gly Ile Asp Gly Gly Gln Pro Trp Arg Arg Ser Phe Gly Asp
81      85      90      95
82 Asn Ile Thr Tyr Thr Asp Trp Arg Arg Asp Asn Phe Tyr Arg Ala Val
83      100     105     110
84 Arg Gln Leu Thr Thr Gly Ala Lys Arg Ile Gly Ile Glu Phe Asp His
85      115     120     125
86 Val Asn Leu Asp Phe Arg Arg Gln Leu Glu Glu Ala Leu Pro Gly Val
87      130     135     140
88 Glu Phe Val Asp Ile Ser Gln Pro Ser Met Trp Met Arg Thr Ile Lys
89      145     150     155     160
90 Ser Leu Glu Glu Gln Lys Leu Ile Arg Glu Gly Ala Arg Val Cys Asp
91      165     170     175
92 Val Gly Gly Ala Ala Cys Ala Ala Ala Ile Lys Ala Gly Val Pro Glu
93      180     185     190
94 His Glu Val Ala Ile Ala Thr Thr Asn Ala Met Ile Arg Glu Ile Ala
95      195     200     205
96 Lys Ser Phe Pro Phe Val Glu Leu Met Asp Thr Trp Thr Trp Phe Gln
97      210     215     220
98 Ser Gly Ile Asn Thr Asp Gly Ala His Asn Pro Val Thr Asn Arg Ile
99      225     230     235     240
100 Val Gln Ser Gly Asp Ile Leu Ser Leu Asn Thr Phe Pro Met Ile Phe
101      245     250     255
102 Gly Tyr Tyr Thr Ala Leu Glu Arg Thr Leu Phe Cys Asp His Val Asp
103      260     265     270
104 Asp Ala Ser Leu Asp Ile Trp Glu Lys Asn Val Ala Val His Arg Arg
105      275     280     285
106 Gly Leu Glu Leu Ile Lys Pro Gly Ala Arg Cys Lys Asp Ile Ala Ile
107      290     295     300
108 Glu Leu Asn Glu Met Tyr Arg Glu Trp Asp Leu Leu Lys Tyr Arg Ser
109      305     310     315     320

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110 Phe Gly Tyr Gly His Ser Phe Gly Val Leu Cys His Tyr Tyr Gly Arg
111           325           330           335
112 Glu Ala Gly Val Glu Leu Arg Glu Asp Ile Asp Thr Glu Leu Lys Pro
113           340           345           350
114 Gly Met Val Val Ser Met Glu Pro Met Val Met Leu Pro Glu Gly Met
115           355           360           365
116 Pro Gly Ala Gly Gly Tyr Arg Glu His Asp Ile Leu Ile Val Gly Glu
117           370           375           380
118 Asp Gly Ala Glu Asn Ile Thr Gly Phe Pro Phe Gly Pro Glu His Asn
119 385           390           395           400
120 Ile Ile Arg Asn
121           404

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123 (2) INFORMATION FOR SEQ ID NO: 2:

125 (i) SEQUENCE CHARACTERISTICS:

126 (A) LENGTH: 1212 base pairs

127 (B) TYPE: nucleic acid

128 (C) STRANDEDNESS: double

129 (D) TOPOLOGY: linear

131 (ii) MOLECULE TYPE: genomic DNA

133 (vi) ORIGINAL SOURCE:

134 (A) ORGANISM: *Alcaligenes faecalis*

135 (B) STRAIN: TE3581 (FERM P-14237)

137 (ix) FEATURE:

138 (A) NAME/KEY: CDS

139 (B) LOCATION: 1 to 1212

141 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

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143 ATG ACT GAC GAC ATG TTG CAC GTG ATG AAA TGG CAC AAC GGC GAG AAA 48
144 Met Thr Asp Asp Met Leu His Val Met Lys Trp His Asn Gly Glu Lys
145 1 5 10 15
146 GAT TAT TCG CCG TTT TCG GAT GCC GAG ATG ACC CGC CGC CAA AAC GAC 96
147 Asp Tyr Ser Pro Phe Ser Asp Ala Glu Met Thr Arg Arg Gln Asn Asp
148 20 25 30
149 GTT CGC GGC TGG ATG GCC AAG AAC AAT GTC GAT GCG GCG CTG TTC ACC 144
150 Val Arg Gly Trp Met Ala Lys Asn Asn Val Asp Ala Ala Leu Phe Thr
151 35 40 45
152 TCT TAT CAC TGC ATC AAC TAC TAT TCC GGC TGG CTG TAC TGC TAT TTC 192
153 Ser Tyr His Cys Ile Asn Tyr Tyr Ser Gly Trp Leu Tyr Cys Tyr Phe
154 50 55 60
155 GGA CGC AAG TAC GGC ATG GTC ATC GAC CAC AAC AAC GCC ACG ACG ATT 240
156 Gly Arg Lys Tyr Gly Met Val Ile Asp His Asn Asn Ala Thr Thr Ile
157 65 70 75 80
158 TCG GCC GGC ATC GAC GGC GGC CAG CCC TGG CGC CGC AGC TTC GGC GAC 288
159 Ser Ala Gly Ile Asp Gly Gly Gln Pro Trp Arg Arg Ser Phe Gly Asp
160 85 90 95
161 AAC ATC ACC TAC ACC GAC TGG CGC CGC GAC AAT TTC TAT CGC GCC GTG 336
162 Asn Ile Thr Tyr Thr Asp Trp Arg Arg Asp Asn Phe Tyr Arg Ala Val
163 100 105 110
164 CGC CAG CTG ACC ACG GGC GCC AAG CGC ATC GGC ATC GAG TTC GAC CAC 384
165 Arg Gln Leu Thr Thr Gly Ala Lys Arg Ile Gly Ile Glu Phe Asp His

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166	115	120	125	
167	GTC AAT CTC GAC TTC CGC CGC CAG CTC GAG GAA GCC CTA CCG GGC GTC	432		
168	Val Asn Leu Asp Phe Arg Arg Gln Leu Glu Glu Ala Leu Pro Gly Val			
169	130 135 140			
170	GAG TTC GTC GAC ATC AGC CAG CCC TCG ATG TGG ATG CGC ACC ATC AAG	480		
171	Glu Phe Val Asp Ile Ser Gln Pro Ser Met Trp Met Arg Thr Ile Lys			
172	145 150 155 160			
173	TCG CTC GAA GAG CAG AAG CTG ATC CGC GAA GGC GCC CGC GTG TGT GAC	528		
174	Ser Leu Glu Glu Gln Lys Leu Ile Arg Glu Gly Ala Arg Val Cys Asp			
175	165 170 175			
176	GTC GGC GGC GCG GCC TGC GCG GCT GCC ATC AAG GCC GGC GTG CCC GAG	576		
177	Val Gly Gly Ala Ala Cys Ala Ala Ile Lys Ala Gly Val Pro Glu			
178	180 185 190			
179	CAT GAA GTG GCG ATC GCC ACC ACC AAT GCG ATG ATC CGC GAG ATC GCC	624		
180	His Glu Val Ala Ile Ala Thr Thr Asn Ala Met Ile Arg Glu Ile Ala			
181	195 200 205			
182	AAA TCG TTC CCC TTC GTG GAG CTG ATG GAC ACC TGG ACC TGG TTC CAG	672		
183	Lys Ser Phe Pro Phe Val Glu Leu Met Asp Thr Trp Thr Trp Phe Gln			
184	210 215 220			
185	TCG GGC ATC AAC ACC GAC GGC GCG CAC AAT CCG GTC ACC AAC CGC ATC	720		
186	Ser Gly Ile Asn Thr Asp Gly Ala His Asn Pro Val Thr Asn Arg Ile			
187	225 230 235 240			
188	GTG CAA TCC GGC GAC ATC CTT TCG CTC AAC ACC TTC CCG ATG ATC TTC	768		
189	Val Gln Ser Gly Asp Ile Leu Ser Leu Asn Thr Phe Pro Met Ile Phe			
190	245 250 255			
191	GGC TAC TAC ACC GCG CTG GAG CGC ACG CTG TTC TGC GAC CAT GTC GAT	816		
192	Gly Tyr Tyr Thr Ala Leu Glu Arg Thr Leu Phe Cys Asp His Val Asp			
193	260 265 270			
194	GAC GCC AGC CTC GAC ATC TGG GAG AAG AAC GTG GCC GTG CAT CGC CGC	864		
195	Asp Ala Ser Leu Asp Ile Trp Glu Lys Asn Val Ala Val His Arg Arg			
196	275 280 285			
197	GGG CTC GAG CTG ATC AAG CCG GGC GCG CGC TGC AAG GAC ATC GCC ATC	912		
198	Gly Leu Glu Leu Ile Lys Pro Gly Ala Arg Cys Lys Asp Ile Ala Ile			
199	290 295 300			
200	GAG CTC AAC GAG ATG TAC CGC GAG TGG GAC CTG CTG AAG TAC CGC TCC	960		
201	Glu Leu Asn Glu Met Tyr Arg Glu Trp Asp Leu Leu Lys Tyr Arg Ser			
202	305 310 315 320			
203	TTC GGC TAT GGC CAC TCC TTC GGC GTG CTG TGC CAC TAC TAC GGT CGC	1008		
204	Phe Gly Tyr Gly His Ser Phe Gly Val Leu Cys His Tyr Tyr Gly Arg			
205	325 330 335			
206	GAG GCC GGC GTG GAG CTG CGC GAG GAC ATC GAC ACC GAG CTG AAG CCC	1056		
207	Glu Ala Gly Val Glu Leu Arg Glu Asp Ile Asp Thr Glu Leu Lys Pro			
208	340 345 350			
209	GGC ATG GTG GTC TCC ATG GAG CCG ATG GTG ATG CTG CCG GAG GGC ATG	1104		
210	Gly Met Val Val Ser Met Glu Pro Met Val Met Leu Pro Glu Gly Met			
211	355 360 365			
212	CCC GGT GCC GGC GGC TAT CGC GAG CAC GAC ATC CTG ATC GTC GGG GAG	1152		
213	Pro Gly Ala Gly Gly Tyr Arg Glu His Asp Ile Leu Ile Val Gly Glu			
214	370 375 380			

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215 GAC GGT GCC GAG AAC ATC ACC GGC TTC CCG TTC GGT CCG GAA CAC AAC 1200
216 Asp Gly Ala Glu Asn Ile Thr Gly Phe Pro Phe Gly Pro Glu His Asn
217 385 390 395 400
218 ATC ATC CGC AAC 1212
219 Ile Ile Arg Asn
220 404
223 (2) INFORMATION FOR SEQ ID NO: 3:
225 (i) SEQUENCE CHARACTERISTICS:
226 (A) LENGTH: 39 base pairs
227 (B) TYPE: nucleic acid
228 (C) STRANDEDNESS: single
229 (D) TOPOLOGY: linear
231 (ii) MOLECULE TYPE: other nucleic acid (synthetic DNA)
233 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
235 CAACATGTCG TCAGTCATAT GTGTTTCCTG TGTGAAATT 39

VERIFICATION SUMMARY

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Input Set : A:\226749.st25 Replacement Sequence Listing.txt

Output Set: N:\CRF4\04272005\J807228A.raw

L:13 M:220 C: Keyword misspelled or invalid format, [(iii) NUMBER OF SEQUENCES:]
L:30 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:31 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:41 M:220 C: Keyword misspelled or invalid format, [(C) REFERENCE/DOCKET NUMBER:]
L:55 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=1